AMENDMENTS TO THE CLAIMS

Listing of Claims

1. (Currently amended) A method for the fermentative production of ~~at least one sulfur-containing fine chemical~~ L-methionine, which comprises the following steps:

   a) ~~fermentation~~ fermenting in a medium cells of ~~a~~ coryneform ~~bacteria culture~~ bacterium *Corynebacterium glutamicum* for producing ~~the desired sulfur-containing fine chemical~~ L-methionine, ~~the~~ said coryneform bacteria expressing at least one heterologous nucleotide sequence which codes for a protein with homoserine O-acetyltransferase (metA) activity, wherein said heterologous nucleotide sequence comprises a nucleotide sequence encoding a metA protein derived from *Corynebacterium diphteriae* having an amino acid sequence as set forth in SEQ ID NO: 2;

   b) ~~concentration of the sulfur-containing fine chemical~~ concentrating L-methionine in the medium or in the bacterial cells, and

   c) ~~isolation of the sulfur-containing fine chemical~~ isolating L-methionine.

2-4. (Cancelled)

5. (Currently amended) ~~A~~ The method as claimed in claim 1, wherein the metA-encoding nucleotide sequence comprises a coding sequence ~~according to~~ as set forth in SEQ ID NO:1~~, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43 and 45 or a nucleotide sequence homologous thereto which codes for a protein with metA activity~~.

6. (Cancelled)

7. (Currently amended) ~~A~~ The method as claimed in claim 1, wherein the coding metA sequence is a DNA or RNA which can be replicated in coryneform bacteria or is stably integrated into the chromosome.

8. (Currently amended) ~~A~~ The method as claimed in claim 7, wherein

a) a bacteria strain transformed with a plasmid vector carrying at least one copy of the coding metA sequence under the control of regulatory sequences is used, or

b) a strain in which the coding metA sequence has been integrated into the bacteria chromosome is used.

9. (Currently amended) ~~A~~ The method as claimed in claim 1, wherein the coding metA sequence is overexpressed.

10. (Currently amended) ~~A~~ The method as claimed in claim 1, wherein bacteria are fermented in which additionally at least one further gene of the biosynthetic pathway of ~~the desired sulfur-containing fine chemical~~ L-methionine has been amplified or mutated such that its activity is not influenced by metabolic metabolites.

11. (Currently amended) ~~A~~ The method as claimed in claim 1, wherein bacteria are fermented in which at least one metabolic pathway, which reduces the production of ~~the desired sulfur-containing fine chemical~~ L-methionine, is at least partially switched off.

12. (Currently amended) ~~A~~ The method ~~as claimed in~~ of claim 1, wherein coryneform bacteria are fermented in which, at the same time, ~~at least one of the genes selected from among~~

~~a) the gene~~ a lysC gene, ~~which encodes an aspartate kinase,~~

~~b) the glyceraldehyde-3-phosphate dehydrogenase-encoding gene gap,~~

~~c) the 3-phosphoglycerate kinase-encoding gene pgk,~~

~~d) the pyruvate carboxylase-encoding gene pyc,~~

~~e) the triose phosphate isomerase-encoding gene tpi,~~

~~f) the methylene tetrahydrofolate reductase-encoding gene metF,~~

~~g) the cystathionine gamma-synthase-encoding gene metB,~~

~~h) the cystathionine gamma-lyase-encoding gene metC,~~

~~i) serine hydroxymethyltransferase-encoding gene glyA,~~

~~j) the O-acetylhomoserine sulfhydrylase-encoding gene metY,~~

~~k) the vitamin B12-dependent methionine synthase-encoding gene metH,~~

~~l) the phosphoserine aminotransferase-encoding gene serC,~~

~~m) the phosphoserine phosphatase-encoding gene serB,~~

~~n) the serine acetyltransferase-encoding gene cysE, and~~

~~o) the gene hom, which encodes a homoserine dehydrogenase,~~

is overexpressed or mutated in such a way that the activity of the corresponding ~~proteins~~ protein is influenced by metabolic metabolites to a smaller extent, if at all, compared to a nonmutated ~~proteins~~ protein.

13. (Cancelled)

14. (Currently amended) ~~A~~ The method ~~as claimed in~~ of claim ~~1~~ 17, wherein ~~microorganisms~~ the coryneform bacterium is of the species ~~Corynebacterium glutamicum are used~~ *Corynebacterium glutamicum*.

15-16. (Cancelled)

17. (New) A method for the production of L-methionine, which comprises the following steps:

a) fermenting in a medium cells of a coryneform bacterium for producing L-methionine, said coryneform bacteria expressing at least one heterologous nucleotide sequence which codes for a protein with homoserine O-acetyltransferase (metA) activity, wherein the heterologous metA-encoding nucleotide sequence is less than 100% homologous to the metA-encoding sequence from *Corynebacterium glutamicum* ATCC 13032;

b) concentrating L-methionine in the medium or in the bacterial cells; and

c) isolating L-methionine.

18. (New) The method of claim 17, wherein the metA-encoding nucleotide sequence comprises a coding sequence as set forth in SEQ ID NO:1.

19. (New) The method of claim 17, wherein the metA-encoding nucleotide sequence codes for a protein with metA activity, said protein comprising an amino acid sequence as set forth in SEQ ID NO: 2 or a fragment of SEQ ID NO: 2 having metA activity.

20. (New) The method of claim 17, wherein the coding metA sequence is a DNA or RNA which can be replicated in coryneform bacteria or is stably integrated into the chromosome.

21. (New) The method of claim 17, wherein

a) a bacteria strain transformed with a plasmid vector carrying at least one copy of the coding metA sequence under the control of regulatory sequences is used, or

b) a strain in which the coding metA sequence has been integrated into the bacteria chromosome is used.

22. (New) The method of claim 17, wherein the coding metA sequence is overexpressed.

23. (New) The method of claim 17, wherein bacteria are fermented in which additionally at least one further gene of the biosynthetic pathway of L-methionine has been amplified or mutated such that its activity is not influenced by metabolic metabolites.

24. (New) A method for the production of L-methionine, which comprises the following steps:

a) fermenting in a medium cells of a coryneform bacterium for producing of L-methionine, said coryneform bacteria expressing at least one heterologous nucleotide sequence which codes for a protein with homoserine O-acetyltransferase (metA) activity, wherein said heterologous nucleotide sequence comprises a nucleotide sequence encoding a metA protein derived from *Corynebacterium diphteriae*;

b) concentrating L-methionine in the medium or in the bacterial cells; and

c) isolating L-methionine.

25. (New) The method of claim 24, wherein the metA-encoding nucleotide sequence comprises a coding sequence as set forth in SEQ ID NO:1.

26. (New) The method of claim 24, wherein the metA-encoding nucleotide sequence codes for a protein with metA activity, said protein comprising an amino acid sequence as set forth in SEQ ID NO: 2 or a fragment of SEQ ID NO: 2 having metA activity.

27. (New) The method of claim 24, wherein the coding metA sequence is a DNA or RNA which can be replicated in coryneform bacteria or is stably integrated into the chromosome.

28. (New) The method of claim 24, wherein

a) a bacteria strain transformed with a plasmid vector carrying at least one copy of the coding metA sequence under the control of regulatory sequences is used, or

b) a strain in which the coding metA sequence has been integrated into the bacteria chromosome is used.

29. (New) The method of claim 24, wherein the coding metA sequence is overexpressed.

30. (New) The method of claim 24, wherein bacteria are fermented in which additionally at least one further gene of the biosynthetic pathway of L-methionine has been amplified or mutated such that its activity is not influenced by metabolic metabolites.

31. (New) The method of claim 24, wherein the coryneform bacterium is of the species *Corynebacterium glutamicum*.